

Population Dynamics: A Computer Model of Discrimination

STEFAN BYRD-KRUEGER

Introduction

Discrimination exists almost ubiquitously in life. It is called both socially despicable and acceptable, politically incorrect and profitable, as well as evolutionarily stable and suicidal. Arguments can be made for a variety of positions on the issue, often with great confidence, yet it is difficult to deliver clear and consistent accounts of discrimination and how it affects its environment. The goal of this project was to provide a controlled analysis of discrimination and to reliably demonstrate its impact on the dynamics of population growth. This was done by simulating populations of simple, sexually reproducing individuals, modeling the progression of genes in the populations, and detailing how the dynamics of this progression were affected by a behavior of discrimination.

Despite the multitude of definitions and manners of discrimination, for the purpose of this project only one will be identified and discussed. There is no violence in this project, thus words and phrases like “domination”, “eliminating”, and “killing off” refer to the favoring of certain genes over others through random, rule-constrained reproduction, and not to any one individual damaging the status and capacities of its peers. Discrimination in this context will mean the act of selecting mates based on common characteristics, and rejecting mates that fail to meet a defined threshold of similarity.

The hypothesis leading up to this project was that a behavior of discrimination in a population would cause that population to divide up into distinct subgroups. Further stipula-

tions were made regarding the composition and behavior of these subgroups, but many of these were not able to be tested. The results of the experiments were sometimes surprising, yet explainable and often informative. In general, all populations tended to ultimately blend into one subgroup, independent of the presence of discriminators. The behavior of discrimination was found to be evolutionarily precarious for those who practice it, yet surprisingly capable of overcoming its risks and prospering despite them. Two different scenarios of linking discrimination to a specific genotype produced very interesting, yet very different dynamics. The most prominent impact of discrimination on a population was found to be a dramatic acceleration of genetic and subgroup domination.

The Program

The question asked before this project was quite simply, “how is a population affected by a behavior of discrimination?” To answer this we needed a population, a method of discrimination, the ability to identify discrimination in a population and its effects on that population, and the ability to observe populations with and without discrimination, repeatedly. These criteria were met with the development of a computer model incorporating all those elements and abilities. The program, the Discrimination Analysis Application, simulates a population through generations, given certain conditions, and records information about the population, such as the expression of genes and the size of various sub-populations.

In studying the effects of discrimination, two major sets of information were collected and considered, the statistics about gene expression and the sizes of various subpopulations. Information about gene expression refers to a percentage of a population exhibiting one of three genotypes (dominant, heterozygous, and recessive) for any given characteristic. The concept of a subpopulation refers to a specific group in which all members share identical characteristics. For example, if humans had only three characteristics – height, eye color, and hair color – one subpopulation of the human race would be tall, green eyed, brown-haired people.

The Model

Every simulation takes place in an environment, called a world, which consists of a series of populations, each representing a new generation through the passage of time. Populations are collections of persons all of the same generation. Each generation is the product of the previous population, that is to say, when one generation ends, the individu-

als mate, produce the next generation, and then expire. Persons themselves are each defined by their gender and a collection of arbitrary characteristics. Characteristics, or traits, are defined by the status of their two alleles, which combine to determine the trait's genotype (and phenotype, since all traits are expressed)

How it Works

Before starting the simulation, several parameters must be set. Changing parameters include how many generations the world should last, how many characteristics each person has, and the Discrimination Threshold, which dictates the behavior of discriminating individuals. Other parameters which were kept constant between simulations were the size of the starting population, and the maximum and minimum population sizes, two points which constrain population size by changing the rate of reproduction.

The simulator starts by creating the world and then spawning the first population. This population is designated "generation 0", and in it, the preset number of persons is created. Each person has a 50% chance of being male or female and is given the set number of characteristics. Each characteristic has two alleles, each of which can be dominant or recessive. In generation 0 these alleles are automatically and randomly set, with a 50% chance of being set to either state. If both alleles are recessive, the recessive genotype is assigned. If both are dominant, the dominant genotype is assigned. And if the two alleles are different, the characteristic exhibits the heterozygous. This process results in a starting population, roughly half female and half male, that on average is 25% recessive, 50% heterozygous and 25% dominant for every trait.

The next step is the selection of mates, which begins the process of creating the next generation. In turn, every male approaches available females at random (though the genders in this process could easily be reversed) and mates with the first match. It is at this point that discrimination introduces its effect. If a person discriminates, upon approaching a female, there will be a test to see how much the two have in common. If the two candidates have enough characteristics in common to match the predetermined Discrimination Threshold, then the two will mate as usual. If, however, the two share fewer traits than the Discrimination Threshold, the male will reject the female and approach another at random until he has mated, or until he finds that there are no acceptable unpaired females, in which case the male will remain single.

Upon completing the mating process, the next generation is created based on certain rules regarding reproduction. A new population is created and populated with the children of the couples from the previous generation. Each child gets its characteristics from its parents by receiving one allele each from its mother and father and having its genotype determined accordingly. The product of this reproduction process, the new “child” population, becomes the current “living” population, while the previous generation, containing the parents, goes dormant, no longer participating in any mating or reproduction.

The number of children in a new population is determined by whether the population is in a growing or a shrinking mode. Typically, the world starts as growing, which means that there are three children per couple, increasing the size of the new generation. This growth continues until the population size reaches a predefined maximum limit, when couples start having only two children per couple. With only two children per couple, each generation is smaller than the previous one, since there are often unequal numbers of males and females, leaving some unmated, and when discrimination exists some individuals may refuse to mate anyone. When the population size goes below the minimum limit, couples are again set back to having three children, and the cycle continues. This cycle constrains population growth and attrition, but also creates occasional bottlenecks in the population size, which accelerate changes in the expression of characteristics in the world.

This cycling process of mating and creating the next generation continues for as long as the simulator is set to run (sometimes thousands of generations). As it runs, statistics about each generation, its genes, and its subpopulations are recorded to a file for later analysis.

Findings

Genetic Domination by Homogeneous Genotypes

One unexpected discovery from this experiment was the unavoidability of domination among genes and subpopulations. Regardless of the presence of discrimination in a population, all genes tended to shift towards being expressed entirely in either the dominant or recessive genotype. Because of this, even in non-discriminating populations, one subpopulation always found its way to supremacy, pushing out all other subpopulations until the subpopulation became the entire population.

It was originally anticipated that the random interactions would keep gene expression relatively stable, particularly in a population without discrimination. However, in every simulation, for every characteristic, either the dominant or the recessive genotype rose to become the only genotype of that characteristic expressed in the population, while the heterozygous genotype was invariably pressed out of the population. Through the process of random mating, one of the two homozygous genotypes (where both alleles are identical) ended up dominating the population.

Though unanticipated, this trend is understandable and can be explained by the mechanics of the model. While the possible outcomes from mixing parents of different genotypes can be complicated, it is important to note that two parents who are both recessive or both dominant for a trait can only produce a child of the parents' genotype. Heterozygous parents, however, can give rise to all three genotypes. Thus, homogeneous populations reinforce themselves in reproduction, while heterogeneous populations will feed into the homogeneous ones. When a homogeneous genotype claims a majority of a population, its self-reinforcement is strengthened, as individuals of that genotype become more likely to mate with other individuals of that genotype, necessarily producing more homogeneous offspring. The result is a favoring of recessive and dominant genotypes, and an unbreakable hold on the population should either genotype achieve dominance.

As a result of the genotype domination, domination also occurs among the subpopulations. Again, subpopulations are defined by their genotypes, so trends among the genotypes will manifest themselves as trends among the subpopulations. When genetic dominance has been achieved by all characteristics, by definition all individuals can only express one genotype for each of their traits. Since a specific subpopulation is defined as a group of individuals who all share the same characteristics, a population in which all individuals are expressing the same genotypes for all traits is comprised of only one subpopulation. This subpopulation has achieved domination.

While domination may occur regardless of the presence of discrimination in a population, discrimination has an undeniable and dramatic effect on the rate of domination. Discrimination compels individuals to choose mates with more of the same characteristics. Thus, an individual who is recessive for a trait will more often mate with someone who is also recessive for that trait, hugely increasing the chance that the child will also be recessive. Without discrimination, the individual would pick randomly, which significantly decreases the chance of this genetic reinforcement. An increased level of discrimination can dramatically increase the rate of genetic drift.

Discrimination Adaptation

During the development of this program, one prediction made was that discriminators would be at a disadvantage, since discriminating individuals who reject potential mates would more often fail to find a mate than their non-discriminating counterparts. Yet in long-term analyses lasting several hundreds or thousands of generations, there appeared to be no difference in population growth rates. After a more careful analysis, it was discovered that in fact there is a disadvantage to discriminating, but discrimination quickly overcomes this, not by adapting to the environment, but by adapting the environment to discrimination.

Discrimination and its effects are more prominent in populations with a high number of characteristics and with a high Discrimination Threshold. Accordingly, a population was created with a relatively high number of characteristics (ten, compared with a usual three) and a high Threshold (eight, compared with a usual max of two), meaning that individuals would only mate with someone they were almost identical too. A Threshold of eight was chosen, because approximately one in ten populations survived, whereas at a Threshold of nine out of ten, even after three hundred simulations, no populations survived for more than three or four generations.

As mentioned, with a threshold of eight, most populations die off, indicating the disadvantage of discrimination, but what happened in the populations that did survive shed light on how moderate discrimination seemed viable in long run. As anticipated, as soon as the population spawns, discrimination causes many individuals to fail to find mates, and most die off in the first mating season. The population continues to plummet, but if the population survives, this decline bottoms out at less than twenty, or even ten individuals. This low is a crucial point in deciding the survival of the population, as even two compatible mates can produce incompatible offspring because of heterozygosity.

This low point, however, serves as an extreme bottleneck, that squeezes difference out of the population, immediately eliminating most genotypes, and ultimately saving discrimination. By the time the population starts to replenish its numbers, there are very few genotypes and subpopulations remaining. Individuals now find that most of the population is very similar to them, and match or exceed their Discrimination Threshold. By the time the population has fully recovered, any individual will happily mate with almost any other individual in the population. By killing off diversity, discrimination has effectively created a

world for itself in which everyone is acceptable. Discrimination has rushed the previously described process of subgroup domination, and therefore individuals no longer exercise their discrimination by rejecting mates. Since the population grows without discrimination, it no longer suffers from the disadvantage of discrimination and continues through population cycles like any other population. Since this genetic attrition happens so rapidly, eliminating most diversity in less than 10 generations, the long-run analysis of population size is unaffected by the discrimination disadvantage.

Discrimination Linked to a Genotype

In studying the effects of discrimination, having compared a population of discriminators to a population without discriminators, we will now consider a mixed population. This mix was achieved by linking the behavior of discrimination to the dominant genotype of an individual's first gene, characteristic 0. Because of this method, approximately 25% of individuals are born as discriminators in the first population. From this starting point simulations were run for two different scenarios with two different sets of rules. In one case, the standard case, all individuals dominant for trait 0 discriminated, and so, discriminators would only mate with someone similar to them. Inadvertently, another set of rules was tested in which discrimination was also sex linked, that is only the males dominant for trait 0 discriminated while females of the discriminating genotype could not discriminate against their suitors and would consent to any mate independent of their own genotypes.

In the standard case, which was originally planned for, discrimination proved fatal to the discriminating population. The discriminating subpopulations face a rapid decline as the dominant genotype for trait 0 was pushed out of the population, and the recessive genotype quickly ascends. The best explanation for this starts with the discrimination disadvantage. Since discriminators can reject available mates, they have a lower chance of producing offspring. Discriminators have the highest chance of producing discriminating children, so this decreases the probability that discriminators will increase. Simultaneously, non-discriminators (heterozygotes and recessives) tend to produce non-discriminating offspring, both because of their natural tendency to do so and because discriminators are less like to choose and accept them as mates, so the population of non-discriminators will increase. Furthermore, should a discriminator accept and mate with a non-discriminator, they will most likely produce a non-discriminating child (50% chance with a heterozygote and 100% chance with a recessive). This reduced probability of producing discriminators,

increased probability of producing non-discriminators, and genetic leakage out of the discriminating population all result in a vanishing discriminator population.

The other linkage scenario, where only males dominant for trait 0 can discriminate, was originally generated through an accident, a slight alteration in the code of the program, but met with drastically different results. Functionally, this alteration created a world in which only males had the power to discriminate. That is, a discriminating male could reject a female who is not similar enough to match his threshold, but a female who is dominant for the discrimination gene would be powerless to reject a non-discriminating male who shares no characteristics with her. The result of this scenario is a rapid ascendance of the discriminating genotype. This trend might be explained by the shift in mating preferences and the changes in gene progression that this shift elicits. The male discriminators in this population still suffer from the discrimination disadvantage by passing up opportunities to mate and pass on their genes. However, the females dominant for the discrimination trait are unable to discriminate, and therefore act as homozygous carriers for the trait (two dominant alleles). Unlike the typical heterozygous carriers (one dominant allele) who are likely to produce non-discriminating children, these dominant carriers are much more likely to produce a discriminating child, and cannot produce the opposite recessive children. Non-discriminators now have a larger chance of mating with someone who is dominant for the discrimination trait, and are therefore more likely to produce new discriminators. While there is still genetic leakage out of the discriminating population from discriminators who accept and mate with non-discriminators, there is now a more significant genetic influx of discriminators from non-discriminators mating with dominant carrier females. Together, the tendency of discriminating males to pick dominant carrier females over other non-discriminators, and the ability of dominant carrier females to readily mate with non-discriminators, producing more discriminators out of the non-discriminating population, might explain the ascendancy of the discrimination genotype in the population.

Conclusions

The clearest and most consistent effect of discrimination on its environment is an acceleration of change. Throughout the analysis of results, the ability of discrimination to accelerate change in a population remained prominent. In all simulations, populations shifted over time, with and without discrimination. Gene expression always polarized so that one genotype and one subpopulation would dominate the population. When discrimination

behavior was linked to a genotype, discrimination would die out in the standard scenarios, and in the sex-linked scenarios discrimination would thrive. Whether these shifts were caused by discrimination or natural trends resulting from random interaction, the greater the degree of discrimination in the population, the faster the shifts were effected.

The impacts of discrimination as detailed in this paper fit intuitively with some common concepts regarding such behavior. For example, it is understood that incestuous behavior can increase the chances of expressing a recessive disorder, such as sickle-cell anemia, or a dominant disorder like Huntington's disease. Discrimination, as put forth in this paper, causes individuals to mate with people who are similar to them, and as family members often share many characteristics, discrimination increases the prevalence of incest. It was demonstrated in this research that such discrimination accelerates a movement towards recessive and dominant genotype expression, corroborating and substantiating the commonly held belief that such behavior can lead to disorders.

This project also produced a basic model that fits what we observe as different ethnicities, or local subgroups among the human population. The model in this paper demonstrated that a diverse yet isolated population that breeds over many generations will tend to blend itself into one dominant subgroup. When we look at the development of the human race, we see that regional populations (i.e. the French, the Polish), which were geographically isolated before the modern age, blended themselves into separate groups with distinct features, so that one could tell them apart just by observation. Though this model does not come near to detailing the nuanced differences between and within ethnicities, the basic principles are echoed in both the simulated and the real worlds.

Despite these similarities, however, it should be well understood that this simulation of discrimination and the conclusions drawn from its study are by no means exhaustive. This model is successful at demonstrating the most basic effect that discriminating behavior can have on a small, isolated, highly simplified population. From it, we can gather intuition and broad understandings about discrimination, but we must be careful about directly comparing or applying this model to any real world societies or situations. There are several directions I would have liked to take this project in, and features I would have liked to add to the program, to make it more applicable and capable of accurately modeling real-life environments.

To start, changing the limits on population size might make a significant difference. The small population of this simulator and the frequently induced bottlenecks in the population likely played a significant role in the speed and abruptness of genetic change. When the population grows very small, it puts genotypes and subpopulations at great risk of dying off. In a model with a larger population, bottlenecking would play less of a role in population dynamics, making it easier to identify changes from other factors, such as discrimination.

It would be interesting to study the impact of giving discriminators the ability to settle for a near substitute in the event that a mate exceeding the Discrimination Threshold cannot be found. This would reduce the impact of the discrimination disadvantage, but also mitigate the domination-reinforcing effect of discrimination. It is difficult to say what, if any, effect this would have on a population, particularly in the long run. In conjunction with other changes in the program, slowing the drastic impacts of discrimination on population dynamics might allow genetic nuances the ability to develop into significant genetic movements.

Another addition might be the ability to introduce point modifications to the population. For example, instead of starting the population with discrimination in the sex linked scenarios, the world might start off with an all recessive non-discriminating population. Then at a given time during the population's progression, one or more dominant alleles could be introduced. It is conceivable that the non-discriminators would randomly pass the allele throughout the population as heterozygotes, and produce a population of discriminators, which would sustain itself, and eventually take over the population. Mid-simulation studies like this could take many forms and demonstrate a variety of outcomes.

One highly intriguing, major reconstruction could address the lack of environmental impacts in the model, such as pressures favoring or endangering certain genes. While in the current program a genotype on the verge of extinction stands little chance of recovery, such a minority might find itself with an evolutionary advantage over the majority. For example, if a minority of tall individuals had access to abundant food supplies in trees, while a short majority would overtax a limited food supply on the ground. Or contrarily, vulnerability could be linked to a gene in the form of a recessive genetic condition, leaving individuals less able to cope with an environmental danger, such as predators. While some of these ideas may prove complicated to enact, modeling real world environments and situations is ever appealing, and serves as a valuable tool in understanding the dynamics of discrimination.

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